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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/538,396DATE: 04/19/2000
TIME: 17:20:17

Input Set: I538396.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1 <110> APPLICANT: Mahajan, Pramod B.
2 Shi, Jinrui
3 <120> TITLE OF INVENTION: Maize Rad50 Orthologue and Uses Thereof
4 <130> FILE REFERENCE: 1116
5 <140> CURRENT APPLICATION NUMBER: US/09/538,396
6 <141> CURRENT FILING DATE: 2000-03-29
7 <150> EARLIER APPLICATION NUMBER: 60/132,575
8 <151> EARLIER FILING DATE: 1999-05-05
9 <160> NUMBER OF SEQ ID NOS: 3
10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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13 <212> TYPE: DNA
14 <213> ORGANISM: Zea mays
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21 ctccactgcc ctccttttc tctttccaat cgttttgcaa tcactacgag cgtaatgaat 180
22 agaagttgat agggagatag catccgcaat ctaggtttgg ggcaatcgct ctggccagac 240
23 tggatcggag tgcaagtcgt agaggaggc acttggggct cgtggggcaa g atg agc 297
24 Met Ser
25 1
26 acc gtt gac aag atg ctg atc aag ggg att cgg agc ttc gat ccg gac 345
27 Thr Val Asp Lys Met Leu Ile Lys Gly Ile Arg Ser Phe Asp Pro Asp
28 5 10 15
29 aat aag aac gtc atc acc ttc ttc aag ccg ctc acc ctc atc gtt ggc 393
30 Asn Lys Asn Val Ile Thr Phe Phe Lys Pro Leu Thr Leu Ile Val Gly
31 20 25 30
32 ccc aac ggt gct ggc aag acc acg atc atc gag tgc ctg aag ctt tct 441
33 Pro Asn Gly Ala Gly Lys Thr Thr Ile Ile Glu Cys Leu Lys Leu Ser
34 35 40 45 50
35 tgc acc ggc gag ctg ccc ccc aac tcc cgc tct ggc cac acc ttc gtc 489
36 Cys Thr Gly Glu Leu Pro Pro Asn Ser Arg Ser Gly His Thr Phe Val
37 55 60 65
38 cac gac ccc aag gta gct ggc gag acg gaa aca aaa gga caa att aag 537
39 His Asp Pro Lys Val Ala Gly Glu Thr Glu Thr Lys Gly Gln Ile Lys
40 70 75 80
41 ttg cgg ttt aag act gca gca gga aag gat gtg gtg tgc atc cgg tcc 585
42 Leu Arg Phe Lys Thr Ala Ala Gly Lys Asp Val Val Cys Ile Arg Ser
43 85 90 95
44 ttc cag ctt acc caa aag gca tca aag atg gag ttt aag gca att gaa 633
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47	agc gtc ctc cag act ata aat cca cac aca ggg gag aaa gtc tgc ctc	681
48	Ser Val Leu Gln Thr Ile Asn Pro His Thr Gly Glu Lys Val Cys Leu	
49	115 120 125 130	
50	agc tac aga tgt gct gac atg gat aga gag att cct gcc tta atg ggt	729
51	Ser Tyr Arg Cys Ala Asp Met Asp Arg Glu Ile Pro Ala Leu Met Gly	
52	135 140 145	
53	gtt tcg aag gcc gta ctg gag aat gtt ata ttt gtt cac caa gat gaa	777
54	Val Ser Lys Ala Val Leu Glu Asn Val Ile Phe Val His Gln Asp Glu	
55	150 155 160	
56	tcc aat tgg cca ttg cag gac ccg tca aca ctt aag aag aag ttc gat	825
57	Ser Asn Trp Pro Leu Gln Asp Pro Ser Thr Leu Lys Lys Lys Phe Asp	
58	165 170 175	
59	gac atc ttc tct gcc aca cgc tat acg aaa gct ctt gaa gtc ata aag	873
60	Asp Ile Phe Ser Ala Thr Arg Tyr Thr Lys Ala Leu Glu Val Ile Lys	
61	180 185 190	
62	aaa ctt cac aag gat caa atg caa gag atc aag act ttt agg tta aag	921
63	Lys Leu His Lys Asp Gln Met Gln Glu Ile Lys Thr Phe Arg Leu Lys	
64	195 200 205 210	
65	ctg gag aac ctt cag act gta aaa gac caa gca cat aag ctg cgt gaa	969
66	Leu Glu Asn Leu Gln Thr Val Lys Asp Gln Ala His Lys Leu Arg Glu	
67	215 220 225	
68	aat att gct caa gat caa gaa aag tca gat gcc tca aaa tct cag atg	1017
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71	gag caa ctg aag gaa aag atc tgt ggt acc gag aga gaa atc ctg caa	1065
72	Glu Gln Leu Lys Glu Lys Ile Cys Gly Thr Glu Arg Glu Ile Leu Gln	
73	245 250 255	
74	atg gaa aca agt ttg gat gaa ctg aga aga ctt cag gga caa att gac	1113
75	Met Glu Thr Ser Leu Asp Glu Leu Arg Arg Leu Gln Gly Gln Ile Asp	
76	260 265 270	
77	atc aag gca aca gag aga agt aca tta ctt acg cag cag cat gaa aag	1161
78	Ile Lys Ala Thr Glu Arg Ser Thr Leu Leu Thr Gln Gln His Glu Lys	
79	275 280 285 290	
80	ctt gct gca ctt tct gag gaa aat gaa gat acc gat gag gaa cta atg	1209
81	Leu Ala Ala Leu Ser Glu Glu Asn Glu Asp Thr Asp Glu Glu Leu Met	
82	295 300 305	
83	gaa tgg caa aca aaa ttt gaa gaa agg att gcg tta cta gaa aca aaa	1257
84	Glu Trp Gln Thr Lys Phe Glu Glu Arg Ile Ala Leu Leu Glu Thr Lys	
85	310 315 320	
86	atc agt aaa ctt gta aga gat atg gat gat gaa gca tct tat agc tcc	1305
87	Ile Ser Lys Leu Val Arg Asp Met Asp Asp Glu Ala Ser Tyr Ser Ser	
88	325 330 335	
89	gtt ctg tcc aaa caa aat tct gaa tta aca cat gaa att gga aag ctc	1353
90	Val Leu Ser Lys Gln Asn Ser Glu Leu Thr His Glu Ile Gly Lys Leu	
91	340 345 350	
92	cag gca gaa gct gat gct cac ctg act atg aag cat gaa cga gac tca	1401
93	Gln Ala Glu Ala Asp Ala His Leu Thr Met Lys His Glu Arg Asp Ser	
94	355 360 365 370	

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97	375 380 385	
98	cat ccc ttt acg aat gat gtt gct atg aac ctt aca aac agg att aaa	1497
99	His Pro Phe Thr Asn Asp Val Ala Met Asn Leu Thr Asn Arg Ile Lys	
100	390 395 400	
101	gcg aga cta tca agt ctt gag aat gat ttg ctg gat aag aag aaa tcc	1545
102	Ala Arg Leu Ser Ser Leu Glu Asn Asp Leu Leu Asp Lys Lys Lys Ser	
103	405 410 415	
104	aat gaa gat cag tta gat gtt ttg tgg aaa cac tat ctt aaa ata aat	1593
105	Asn Glu Asp Gln Leu Asp Val Leu Trp Lys His Tyr Leu Lys Ile Asn	
106	420 425 430	
107	gct cgc tac tcc gaa gtt gat ggt cag ata caa tct aag att gaa tcc	1641
108	Ala Arg Tyr Ser Glu Val Asp Gly Gln Ile Gln Ser Lys Ile Glu Ser	
109	435 440 445 450	
110	atg tca ggc att tta aga cgg aga aaa gat aaa gag aaa gaa cgc gat	1689
111	Met Ser Gly Ile Leu Arg Arg Arg Lys Asp Lys Glu Lys Glu Arg Asp	
112	455 460 465	
113	gct gca gaa gtg gag ctt tca aaa ttt aat cta tcc cgt atc gat gag	1737
114	Ala Ala Glu Val Glu Leu Ser Lys Phe Asn Leu Ser Arg Ile Asp Glu	
115	470 475 480	
116	agg gag aga cat atg caa att gaa gtc gag agg aag aca ctt gcg ctt	1785
117	Arg Glu Arg His Met Gln Ile Glu Val Glu Arg Lys Thr Leu Ala Leu	
118	485 490 495	
119	gga gaa aga gac tat gat tca att ata agt cag aaa cga aca gaa gta	1833
120	Gly Glu Arg Asp Tyr Asp Ser Ile Ile Ser Gln Lys Arg Thr Glu Val	
121	500 505 510	
122	tat agt ttg gaa cag aaa ata aaa gtg ctt ctg ccg gag aaa gat ata	1881
123	Tyr Ser Leu Glu Gln Lys Ile Lys Val Leu Leu Arg Glu Lys Asp Ile	
124	515 520 525 530	
125	ata aat aga aat gct gat gaa aga gta aaa ctg ggt ttg aag aag gat	1929
126	Ile Asn Arg Asn Ala Asp Glu Arg Val Lys Leu Gly Leu Lys Lys Asp	
127	535 540 545	
128	gca ttg gaa agc agc aag gac aag ctc aat gag ata gtt aat gag cat	1977
129	Ala Leu Glu Ser Ser Lys Asp Lys Leu Asn Glu Ile Val Asn Glu His	
130	550 555 560	
131	aag gat aaa atc aaa aag gta ctt agg ggg agg aat cct ttt gag aag	2025
132	Lys Asp Lys Ile Lys Lys Val Leu Arg Gly Arg Asn Pro Phe Glu Lys	
133	565 570 575	
134	gat atg aag aag gag atc aat caa gcc ttt tgg cct gtg gac aag gaa	2073
135	Asp Met Lys Lys Glu Ile Asn Gln Ala Phe Trp Pro Val Asp Lys Glu	
136	580 585 590	
137	tac aat gag tta aga tca aaa tcc cag gaa gca gag caa gag ctt aaa	2121
138	Tyr Asn Glu Leu Arg Ser Lys Ser Gln Glu Ala Glu Gln Glu Leu Lys	
139	595 600 605 610	
140	ttt act cag agc aaa gta act gat gct aga gaa caa ttg aca aaa ctt	2169
141	Phe Thr Gln Ser Lys Val Thr Asp Ala Arg Glu Gln Leu Thr Lys Leu	
142	615 620 625	
143	cga aga gat atg gat gca aaa aga aga ttc ctg gac tcg aaa ctt caa	2217
144	Arg Arg Asp Met Asp Ala Lys Arg Arg Phe Leu Asp Ser Lys Leu Gln	

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197	ctg att gta gaa aag aag ctt tta gaa gag tct ctt gat cca ttg tcc	3081
198	Leu Ile Val Glu Lys Lys Leu Leu Glu Glu Ser Leu Asp Pro Leu Ser	
199	915 920 925 930	
200	aaa gag aaa gag agc ttg ttg caa gag tat aat gct ttg aag caa aag	3129
201	Lys Glu Lys Glu Ser Leu Leu Gln Glu Tyr Asn Ala Leu Lys Gln Lys	
202	935 940 945	
203	ctg gat gaa gag tat cat cag ctt gca gaa aga aaa agg gag ttc cag	3177
204	Leu Asp Glu Glu Tyr His Gln Leu Ala Glu Arg Lys Arg Glu Phe Gln	
205	950 955 960	
206	caa gaa ctt gat gct ctt gga aga ctt aat atg aag ata aaa ggg tac	3225
207	Gln Glu Leu Asp Ala Leu Gly Arg Leu Asn Met Lys Ile Lys Gly Tyr	
208	965 970 975	
209	ttg gat tcc aag aaa aac gaa aag ctt aag gaa ttg cag gga agg cat	3273
210	Leu Asp Ser Lys Lys Asn Glu Lys Leu Lys Glu Leu Gln Gly Arg His	
211	980 985 990	
212	gtt ctt tgc cat tct cag tta cag agt tgc atg gca aaa cag caa aga	3321
213	Val Leu Cys His Ser Gln Leu Gln Ser Cys Met Ala Lys Gln Gln Arg	
214	995 1000 1005 1010	
215	ata tca gct gag tta aac aag agc aaa gaa cta ctg cag ggc cag ggc	3369
216	Ile Ser Ala Glu Leu Asn Lys Ser Lys Glu Leu Leu Gln Gly Gln Gly	
217	1015 1020 1025	
218	cag ttg aaa aga aac att gat gac aat ctc aag tac agg aaa aca aag	3417
219	Gln Leu Lys Arg Asn Ile Asp Asp Asn Leu Lys Tyr Arg Lys Thr Lys	
220	1030 1035 1040	
221	gct gat gtg gaa caa ctt act cgt gat ata gaa tca ctt gaa gaa agg	3465
222	Ala Asp Val Glu Gln Leu Thr Arg Asp Ile Glu Ser Leu Glu Glu Arg	
223	1045 1050 1055	
224	ctg ctt tca ata ggt agc ttg tct gct ata gaa gct gat ctg aaa cgc	3513
225	Leu Leu Ser Ile Gly Ser Leu Ser Ala Ile Glu Ala Asp Leu Lys Arg	
226	1060 1065 1070	
227	cat tct caa gaa aaa gag agg ctt aat tca gaa ttt aac agg tgg caa	3561
228	His Ser Gln Glu Lys Glu Arg Leu Asn Ser Glu Phe Asn Arg Trp Gln	
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230	gga aca ctt tct gtt tat caa agt aat att tca aag cac aaa caa gag	3609
231	Gly Thr Leu Ser Val Tyr Gln Ser Asn Ile Ser Lys His Lys Gln Glu	
232	1095 1100 1105	
233	ctt aaa ctg tca cag tac aag gat atc gag aag cga tat act aat caa	3657
234	Leu Lys Leu Ser Gln Tyr Lys Asp Ile Glu Lys Arg Tyr Thr Asn Gln	
235	1110 1115 1120	
236	ttt ctc cag ctt aag aca act gaa atg gca aac aag gac ttg gac aga	3705
237	Phe Leu Gln Leu Lys Thr Thr Glu Met Ala Asn Lys Asp Leu Asp Arg	
238	1125 1130 1135	
239	tat tat act gct tta gac aag gct ctt atg cgg ttc cac agc atg aag	3753
240	Tyr Tyr Thr Ala Leu Asp Lys Ala Leu Met Arg Phe His Ser Met Lys	
241	1140 1145 1150	
242	atg gag gag ata aat aaa ata atc aag gaa ctg tgg caa cag aca tac	3801
243	Met Glu Glu Ile Asn Lys Ile Ile Lys Glu Leu Trp Gln Gln Thr Tyr	
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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
